

Alignment 1

RESULT 11
 ID R15141 standard; Protein; 344 AA.
 AC R15141;
 DT 24-FEB-1992 (first entry)
 DE RecA.
 KW Recombinant repair; amplification.
 OS Aquaspirillum magnetotacticum.
 PN W09117267-A.
 PD 14-NOV-1991.
 PF 17-APR-1991; U02626.
 PR 07-MAY-1990; US-520321.

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lmod.rag

PA (STRI) SRI INTERNATIONAL.
 PI Zarling DA, Sena EP, Green CJ;
 DR WPI; 91-353786/48.
 DR N-PSDB; Q14781.
 PT Amplification of target DNA sequences - using primers, RecA
 protein, ATP-gamma-S, dNTPs and DNA polymerase.
 PS Example 10; Fig 13; 52pp; English.
 CC DNA encoding the sequence, plus a further 800 bp of uncharacterised
 CC genomic DNA, was used as a probe to identify and clone the Thermus
 CC aquaticus RecA gene. The heat stable RecA protein encoded by the T.
 CC aquaticus gene can be used in a new method for the amplification of
 CC target DNA sequences. The RecA protein strongly facilitates hybridis-
 CC ation of the primers to the DNA and prepn. of the primer-target com-
 CC plex topologically for extension by the polymerase. ATP-gamma-S acts
 CC as a cofactor in strand transfer. The reaction may be carried out at a
 CC temp. above 50 deg. C and below the temp. required for thermal dis-
 CC sociation of the target strands and primers. The RecA coated primers
 CC may be useful as probes in diagnostic systems.
 SQ Sequence 344 AA;

Query Match 70.7%; Score 99; DB 1; Length 344;
 Best Local Similarity 46.2%; Pred. No. 5.22e-02;
 Matches 12; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

Db 38 VSTRILGLDVALGIGGVPGGRIIEVY 63
 :|| |:||:| :| ||:|
 Qy 1 ISTXSLSLDIALXXXXLPMXRIVEIY 26

Alignment 2

sp|P95526|RECA_PASMU RECA PROTEIN >gi|1772591|emb|CAA67699.1| (X99324)

RecA protein

[Pasteurella multocida]

Length = 354

Score = 49.2 bits (115), Expect = 5e-06

Identities = 22/26 (84%), Positives = 25/26 (95%)

Query: 1 ISTGSLSLDIALGAGGLPMGRIVEIY 26

+STGSLSLD+ALG GGLPMGRIVEI+

Sbjct: 41 VSTGSLSLDVALGIGGLPMGRIVEIF 66

↑

↑

1: P95526. RECA PROTEIN...[gi:3219853]
 LOCUS RECA_PASMU 354 aa BCT 15-FEB-2000 A2 4/27
 DEFINITION RECA_PROTEIN.
 ACCESSION P95526
 PID g3219853
 VERSION P95526 GI:3219853
 DBSOURCE swissprot: locus RECA_PASMU, accession P95526;
 class: standard.
 → created: Jul 15, 1998.
 sequence updated: Jul 15, 1998.
 annotation updated: Feb 15, 2000.
 xrefs: gi: 1772590, gi: 1772591
 xrefs (non-sequence databases): HSSP P03017, PFAM PF00154, PROSITE
 PS00321
 KEYWORDS DNA damage; DNA recombination; SOS response; ATP-binding;
 DNA-binding.
 SOURCE Pasteurella multocida.
 ORGANISM Pasteurella multocida
 Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
 Pasteurella.
 REFERENCE 1 (residues 1 to 354)
 AUTHORS Barbe Garcia, J.
 TITLE Direct Submission
 → JOURNAL Submitted (??-JUL-1996) to the EMBL/GenBank/DDBJ databases
 REMARK SEQUENCE FROM N.A.
 STRAIN=2,5
 COMMENT

 This SWISS-PROT entry is copyright. It is produced through a
 collaboration between the Swiss Institute of Bioinformatics and
 the EMBL outstation - the European Bioinformatics Institute.
 The original entry is available from <http://www.expasy.ch/sprot>
 and <http://www.ebi.ac.uk/sprot>

[FUNCTION] RECA PROTEIN CAN CATALYZE THE HYDROLYSIS OF ATP IN THE
 PRESENCE OF SINGLE-STRANDED DNA, THE ATP-DEPENDENT UPTAKE OF
 SINGLE-STRANDED DNA BY DUPLEX DNA, AND THE ATP-DEPENDENT
 HYBRIDIZATION OF HOMOLOGOUS SINGLE-STRANDED DNAs. IT INTERACTS WITH
 LEXA CAUSING ITS ACTIVATION AND LEADING TO ITS AUTOCATALYTIC
 CLEAVAGE.

[SIMILARITY] BELONGS TO THE RECA FAMILY.

FEATURES Location/Qualifiers
 source 1..354
 /organism="Pasteurella multocida"
 /db_xref="taxon:747"
 Protein 1..354
 /product="RECA PROTEIN"
 Site 67..74
 /site_type="np-binding"
 /note="ATP (POTENTIAL)."

ORIGIN

1 matkeeknka laaalgqiek qfgkgsimkl gdtqaldvea vstgslsldv algigglpmg
 61 riveifgpes sgkttltlsv iaqaqkegkt cafidaehal dpiyaaklgv nvnellvsqp
 121 dngeqaleic dalvrsgavd viivdsvaal tpkaeiegem gdshmgqlqar lmsqalrklt
 181 gqiknsnclv vfinqirmki gvmfgnpett tggnaikfya svrldirrtg aikegeevig
 241 netrvkvvkn kvaapfrqvd fqilygggis ktgelielgv khklvdkaga wyayngekig
 301 qgkanamkwI eehpeealal etklrnella npekvlaadi aeknesstgl eady

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Alignment 3

gb|AAC16335.1| (AF062380) Dmcl homolog [Leishmania major]
Length = 364

Score = 28.9 bits (63), Expect = 6.6
Identities = 13/26 (50%), Positives = 16/26 (61%)

Query: 1 ISTGSLSLDIALGAGGLPMGRIVEIY 26
ISTGS +LD LG GG+ I E +
Sbjct: 126 ISTGSTALDQLLGGGGIESRSITEAF 151

↑



PubMed	Nucleotide	Protein	Genome	Structure	PopSet
Search <u>Protein</u> <input type="checkbox"/> for _____					
<input type="button" value="Go"/> <input type="button" value="Clear"/>					
<input type="button" value="Limits"/>		<input type="button" value="Preview/Index"/>		<input type="button" value="History"/>	
<input type="button" value="Clipboard"/>					

Display	<u>GenPept</u> <input type="checkbox"/>	<input type="button" value="Save"/>	<input type="button" value="Text"/>	<input type="button" value="Add to Clipboard"/>
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☐ 1 : AAC16335 . (AF062380) Dmc1 ho...[gi:3132711]

[Related Sequences](#), [Nucleotide](#)

LOCUS AAC16335 364 aa INV 14-MAY-1998
DEFINITION Dmc1 homolog [Leishmania major].
ACCESSION AAC16335
PID g3132711
VERSION AAC16335.1 GI:3132711
DBSOURCE locus AF062380 accession AF062380.1
KEYWORDS .
SOURCE Leishmania major.
ORGANISM Leishmania major
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
Leishmania.
REFERENCE 1 (residues 1 to 364)
AUTHORS McKean, P.G. and Benson, F.E.
TITLE Direct Submission
JOURNAL Submitted (30-APR-1998) Biochemistry, Imperial College of Science,
Technology and Medicine, London, Herts. SW7 2AZ, UK
COMMENT Method: conceptual translation supplied by author.
FEATURES
Location/Qualifiers
source 1..364
/organism="Leishmania major"
/strain="Friedlin"
/db_xref="taxon:5664"
/chromosome="35"
Protein 1..364
/product="Dmc1 homolog"
CDS 1..364
/gene="DMC1"
/coded_by="AF062380.1:1..1095"
ORIGIN
1 mqqqqqqqqrq hsshfaeerv gdrgaafaep qplhnsvtge aagqsllve rlaehgigaa
61 ditklkqagi ftvpgvqmc rkdliqikgl seakvdkiie aarrvsevgf itgssclqqr
121 stllristgs talldllggg giesrsitea fgeftrgtq ightlcvtcq lplemggng
181 kavyvdtegt frperirpia erfmdsnsv ldnilvaray theqhahlls mvaakmaedq
241 fsllvdsit alfrvdfsg gelaerqqkl akmlsqliki aeefniavyi tnqvvsdpqg
301 asmfvadpkk pvgghilaha sttrlslrkg rgdqrvc kif dspslpelec vysiseqgii
361 dave
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Display	<u>GenPept</u> <input type="checkbox"/>	<input type="button" value="Save"/>	<input type="button" value="Text"/>	<input type="button" value="Add to Clipboard"/>
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Revised: January 10, 2000.

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Alignment 4

pir||RQBCAT recombination protein recA - Thiobacillus ferrooxidans
Length = 346

Score = 44.9 bits (104), Expect = 1e-04
Identities = 21/26 (80%), Positives = 22/26 (83%)

Query: 1 ISTGSLMLDNLGAGGLPMGRIVEIY 26
STGSL LD ALG GGLP GR+VEIY
Sbjct: 40 YSTGSLGLDLALGVGGLPRGRVVEIY 65
↑



PubMed	Nucleotide	Protein	Genome	Structure	PopSet
Search <input type="text" value="Protein"/> for <input type="text"/>					
<input type="button" value="Go"/> <input type="button" value="Clear"/>					
<input type="button" value="Limits"/>		<input type="button" value="Preview/Index"/>		<input type="button" value="History"/>	
<input type="button" value="Clipboard"/>					

Display <input type="text" value="GenPept"/>	<input type="button" value="Save"/>	<input type="button" value="Text"/>	<input type="button" value="Add to Clipboard"/>
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☐ 1 : RQBCAT . recombination prot...[gi:72986]

PubMed, Related Sequences

LOCUS RQBCAT 346 aa BCT 05-MAR-1999
 DEFINITION recombination protein recA - *Thiobacillus ferrooxidans*.
 ACCESSION RQBCAT
 PID g72986
 VERSION RQBCAT GI:72986
 DBSOURCE pir: locus RQBCAT;
 summary: #length 346 #molecular-weight 37096 #checksum 5119;
 genetic: #gene recA;
 superfamily: recombination protein recA;
 PIR dates: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 05-Mar-1999.

KEYWORDS ATP; DNA binding; DNA recombination; DNA repair; P-loop; SOS response.

SOURCE *Thiobacillus ferrooxidans*.

ORGANISM *Thiobacillus ferrooxidans*

Bacteria; Proteobacteria; gamma subdivision.

REFERENCE 1 (residues 1 to 346)

AUTHORS Ramesar, R.S., Abratt, V., Woods, D.R. and Rawlings, D.E.

→ TITLE Nucleotide sequence and expression of a cloned *Thiobacillus ferrooxidans* recA gene in *Escherichia coli*

→ JOURNAL Gene 78 (1), 1-8 (1989)

MEDLINE 89357486

FEATURES Location/Qualifiers
 source 1..346
 /organism="Thiobacillus ferrooxidans"
 /db_xref="taxon:920"
 Protein 1..346
 /product="recombination protein recA"
 /note="recombinase A"
 Region 66..73
 /region_name="region"
 /note="nucleotide-binding motif A (P-loop)"
 Site 72
 /site_type="binding"
 /note="ATP (Lys)"
 Region 140..145
 /region_name="region"
 /note="nucleotide-binding motif B"

ORIGIN

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1 mdeqrskgls aalsqidkqf gkgavmrlgd hnaikdievy stgslgldla lgvvgglprgr
61 vveiygpess gkttltlhai ascqaaggtg afidaehald pgyahklgvd lenllisqpd
121 tgeqaleiad mlvrsgavdl ividsvaalt pkaeiegemg dshvgkqarl msqalrnltg
181 nisrsntlvi finqirmkig vmygspettg ggnalkfyas vrlidirriga ikksdevvgn
241 dtrvkvvknk vappfreaf aiyygegiss lseldvlgvl fdiveksgaw ysyqghrigq
301 gkdnarqylk vhpelaanie qrraaaaagh plafaeeyes pqrssas

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